

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LI, Limin
COHEN, Stanley N
- (ii) TITLE OF INVENTION: MAMMALIAN TUMOR SUSCEPTIBILITY GENES AND THEIR USES
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
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(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-1
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: SHERWOOD, Pamela J.
(B) REGISTRATION NUMBER: 36,677
(C) REFERENCE/DOCKET NUMBER: A62783-1/BIR/PJS
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 61..1203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCCCTCTGCC TGTGGGGACG GAGGAGCGCG CCATGGCTGT CCGAGAGTCA GCTGAAGAAG

AAT; ATG; TGT; AAG TAC AAA TAT AGA GAT CTA ACC GTC CGT CAA ACT GTC Met Met Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Gln Thr Val 1 5 10 15	108
AAT GTC ATC GCT ATG TAC AAA GAT CTC AAA CCT GTA TTG GAT TCA TAT Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr 20 25 30	156
GTT TTT AAT GAT GGC AGT TCC AGG GAG CTG GTG AAC CTC ACT GGT ACA Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr 35 40 45	204
ATC CCA GTG CGT TAT CGA GGT AAT ATA TAT AAT ATT CCA ATA TGC CTG Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu 50 55 60	252
TGG CTG CTG GAC ACA TAC CCA TAT AAC CCC CCT ATC TGT TTT GTT AAG Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys 65 70 75 80	300
CCT ACT AGT TCA ATG ACT ATT AAA ACA GGA AAG CAT GTG GAT GCA AAT Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn 85 90 95	348
GGG AAA ATC TAC CTA CCT TAT CTA CAT GAC TGG AAA CAT CCA CGG TCA Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser 100 105 110	396
GAG TTG CTG GAG CTT ATT CAA ATC ATG ATT GTG ATA TTT GGA GAG GAG Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu 115 120 125	444
CCT CCA GTG TTC TCC CGG CCT ACT GTT TCT GCA TCC TAC CCA CCA TAC Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr 130 135 140	492
ACA GCA ACA GGG CCA CCA AAT ACC TCC TAC ATG CCA GGC ATG CCA AGT Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser 145 150 155 160	540
GGA ATC TCT GCA TAT CCA TCT GGA TAC CCT CCC AAC CCC AGT GGT TAT Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr 165 170 175	588
CCT GGC TGT CCT TAC CCA CCT GCT GGC CCA TAC CCT GCC ACA ACA AGC Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser 180 185 190	636
TCA CAG TAC CCT TCC CAG CCT GTG ACC ACT GTT GGT CCC AGC AGA Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg 195 200 205	684
GAT GGC ACA ATC AGT GAG GAC ACT ATC CGT GCA TCT CTC ATC TCA GCA Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala 210 215 220	732
GTC AGT GAC AAA CTG AGA TGG CGG ATG AAG GAG GAA ATG GAT GGT GCC Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala 225 230 235 240	780
CAG GCA GAG CTT AAT GCC TTG AAA CGA ACA GAG GAA GAT CTG AAA AAA Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys	828

GGC CAC CAG AAA CTG GAA GAG ATG GTC ACC CGC TTA GAT CAA GAA GTA Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val	245	250	255	
260		265	270	876
GCT GAA GTT GAT AAA AAC ATA GAA CTT TTG AAA AAG AAG GAT GAA GAA Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Asp Glu Glu	275	280	285	924
295				972
CTA AGT TCT GCT CTG GAG AAA ATG GAA AAT CAA TCT GAA AAT AAT GAT Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp	290	295	300	
305				1020
ATT GAT GAA GTT ATC ATT CCC ACA GCC CCA CTG TAT AAA CAG ATT CTA Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu	310	315	320	
325				1068
AAT CTG TAT GCA GAG GAA AAT GCT ATT GAA GAC ACT ATC TTT TAC CTT Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu	325	330	335	
340				1116
GGA GAA GCT TTG CGG CGG GGA GTC ATA GAC CTG GAT GTG TTC CTG AAA Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys	345	350		
355				1164
CAC GTC CGC CTC CTG TCC CGT AAA CAG TTC CAG CTA AGG GCA CTA ATG His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met	360	365		
370				1213
CAA AAG GCA AGG AAG ACT GCG GGC CTT AGT GAC CTC TAC TGACATGTGC Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr	375	380		
380				1273
TGTCAGCTGG AGACCGACCT CTCCGAAAG CATTCTTTTC TTCTTCTTT TCTCATCAGT				
AGAACCCACA ATAAGTTATT GCAGTTATC ATTCAAGTGT TAAATATTT GAATCAATAA				1333
TATATTTCT GTTCCTTTG GGTAAAAACT GGCTTTATT AATGCACCTT CTACCCCTTG				1393
TAAGCGTCTG TGCTGTGCTG GGACTGACTG GGCTAAATAA AATTTGTTGC ATAAA				1448

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
20 25 30

Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr
35 40 - 45

Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu
50 55 60

Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
65 70 75 80

Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
85 90 95

Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser
100 105 110

Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu
115 120 125

Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr
130 135 140

Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser
145 150 155 160

Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr
165 170 175

Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser
180 185 190

Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg
195 200 205

Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala
210 215 220

Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala
225 230 235 240

Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys
245 250 255

Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val
260 265 270

Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Asp Glu Glu
275 280 285

Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
290 295 300

Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
305 310 315 320

Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
325 330 335

Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
340 345 350

His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
355 360 365

Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
370 375 380

(i) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 120..1259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGGGGTG TCGATTGTG TGGGACGGTC TGGGGCAGCC ACAGCGGCTG ACCNCNTNGC	60
CTGCAGGGAA GGGAGTCGCC AGGGCCCGTC ATCGGGTGTG GGAGAGCCAG CTCAAGAAAA	120
TGGTGTCCAA GTACAAATAC AGAGACCTAA CTGTACGTGA AACTGTCAAT GTTATTACTC	180
TATACAAAGA TCTCAAACCT GTTTGGATT CATATTTT TAACGATGGC AGTTCCAGGG	240
AACTAATGAA CCTCACTGGA ACAATCCCTG TGCCCTTATAG AGGTAATACA TACAATATTC	300
CAATATGCCT ATGGCTACTG GACACATACC CATATAATCC CCCTATCTGT TTTGTTAACG	360
CTACTAGTTC AATGACTATT AAAACAGGAA AGCATGTTGA TGCAAATGGG AAGATATATC	420
TTCCCTTATCT ACATGAATGG AAACACCCAC AGTCAGACTT GTTGGGGCTT ATTCAAGGTCA	480
TGATTGTGGT ATTTGGAGAT GAACCTCCAG TCTCTCTCG TCCTATTTCG GCATCCTATC	540
CGCCATACCA GGCAACGGGG CCACCAAATA CTTCTACAT GCCAGGCATG CCAGGTGGAA	600
TCTCTCCATA CCCATCCGGA TACCCCTCCA ATCCCAGTGG TTACCCAGGC TGTCCTTACC	660
CACCTGGTGG TCCATATCCT GCCACAACAA GTTCTCAGTA CCCTTCTCAG CCTCCTGTGA	720
CCACTGTGTTG TCCCAGTAGG GATGGCACAA TCAGCGAGGA CACCATCCGA GCCTCTCTCA	780
TCTCTGCGGT CAGTGACAAA CTGAGATGGC GGATGAAGGA GGAAATGGAT CGTGCCCAGG	840
CAGAGCTCAA TGCCTTGAAA CGAACAGAAG AAGACCTGAA AAAGGGTCAC CAGAAACTGG	900
AAGAGATGGT TACCCGTTTA GATCAAGAAG TAGCCGAGGT TGATAAAAAC ATAGAACTTT	960
TGAAAAAGAA GGATGAAGAA CTCAGTTCTG CTCTGGAAA AATGGAAAAT CAGTCTGAAA	1020
ACAATGATAT CGATGAAGTT ATCATTCCCA CAGCTCCCTT ATACAAACAG ATCCTGAATC	1080
TGTATGCAGA AGAAAACGCT ATTGAAGACA CTATCTTTA CTTGGGAGAA GCCTTGAGAA	1140
GGGGCGTGAT AGACCTGGAT GTCTTCTGA AGCATGTACG TCTTCTGTCC CGTAAACAGT	1200
TCCAGCTGAG GGCACATAATG CAAAAAGCAA GAAAGACTGC CGGTCTCAGT GACCTCTACT	1260
GACTTCTCTG ATACCAGCTG GAGGTTGAGC TCTTCTTAAA GTATTCTCT CTTCCCTTTA	1320
TCAGTAGGTG CCCAGAAATAA GTTATTGCAG TTTATCATTC AAGTGTAAAA TATTTGAAT	1380

CAATAATATA TTTCTGTTT TCTTTGGTA AAGACTGGCT TTTATTAATG CACTTCTAT

1440

CCTCTGAAA CTTTTGTGC TGAATGTTGG GACTGCTAAA TAAAATTGT TTTT

1494

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Ser Lys Tyr Lys, Tyr Arg Asp Leu Thr Val Arg Glu Thr Val
1 5 10 15

Asn Val Ile Thr Leu Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
20 25 30

Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Met Asn Leu Thr Gly Thr
35 40 45

Ile Pro Val Pro Tyr Arg Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu
50 55 60

Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
65 70 75 80

Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
85 90 95

Gly Lys Ile Tyr Leu Pro Tyr Leu His Glu Trp. Lys His Pro Gln Ser
100 105 110

Asp Leu Leu Gly Leu Ile Gln Val Met Ile Val Val Phe Gly Asp Glu
115 120 125

Pro Pro Val Phe Ser Arg Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln
130 135 140

Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Gly Gly
145 150 155 160

Ile Ser Pro Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro
165 170 175

Gly Cys Pro Tyr Pro Pro Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser
180 185 190

Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg Asp
195 200 205

Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala Val
210 215 220

Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Arg Ala Gln
225 230 235 240

Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly
245 250 255

His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val Ala
260 265 270

Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Asp Glu Glu Leu
275 280 285

Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp Ile
290 295 300

Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn
305 310 315 320

Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly
325 330 335

Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys His
340 345 350

Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met Gln
355 360 365

Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Thr His Leu Ala Met Asx Asp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Phe Xaa Asn Gly Ala Leu Glx Cys Tyr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGUCAUGAU UGUGGUAUUU GGAGAUG

27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAUCUCCAAA UACCACAAUC AUGACCU

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAUCAUCAUC AUGAGGTGGC TTATGAGTAT TTCTTCCAG

39

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CUACUACUAC UACACCTTT GAGCAAGTTC AGCCTGGTT

39

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGATACCAAG CTGGAGGTG AGCTCTTC

28

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATTTAGCAGT CCCAACATTC AGCACAAA

28

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGACCGACC TCTCCGTAAA GCATTCTT

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAGCCCCAGTC AGTCCCAGCA CAGCACAG

28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATTTAGCAGT CCCAACATTC AGCACAAA

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCTTCTGGG TGGCAGTGAT GGCAT

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGGTGTCGG AGAGCCAGCT CAAGAAA

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTTACCCAC CTGGTGGTCC ATATCCTG

28

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTCCAGCTG GTATCAGAGA AGTCGT

26

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CACAGTCAGA CTTGTTGGGG CTTATTG

27